

## SEQUENCE LISTING

<110> Long, Li  
 Luqman, Mohammad  
 Yabannavar, Asha  
 Zaror, Isabel

<120> USE OF ANTAGONISTIC ANTI-CD40 ANTIBODIES  
 FOR TREATMENT OF AUTOIMMUNE AND INFLAMMATORY DISEASE AND ORGAN  
 TRANSPLANT REJECTION

<130> PP23725.001 (284072)

<150> 60/565,710

<151> 2004-04-27

<150> 60/525,579

<151> 2003-11-26

<150> 60/517,337

<151> 2003-11-04

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for light chain of CHIR-12.12  
 human anti-CD40 antibody

<221> CDS

<222> (1)...(720)

<400> 1

atg	gcg	ctc	cct	gct	cag	ctc	ctg	ggg	ctg	cta	atg	ctc	tgg	gtc	tct	48
Met	Ala	Leu	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Met	Leu	Trp	Val	Ser	
1				5				10						15		

gga	tcc	agt	ggg	gat	att	gtg	atg	act	cag	tct	cca	ctc	tcc	ctg	acc	96
Gly	Ser	Ser	Gly	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Thr	
			20					25						30		

gtc	acc	cct	gga	gag	ccg	gcc	tcc	atc	tcc	tgc	agg	tcc	agt	cag	agc	144
Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	
		35				40						45				

ctc	ctg	tat	agt	aat	gga	tac	aac	tat	ttg	gat	tgg	tac	ctg	cag	aag	192
Leu	Leu	Tyr	Ser	Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	
	50				55					60						

cca	ggg	cag	tct	cca	cag	gtc	ctg	atc	tct	ttg	ggt	tct	aat	cgg	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Val	Leu	Ile	Ser	Leu	Gly	Ser	Asn	Arg	Ala	
65					70					75					80	

tcc	ggg	gtc	cct	gac	agg	ttc	agt	ggc	agt	gga	tca	ggc	aca	gat	ttt	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				85				90						95		

aca	ctg	aaa	atc	agc	aga	gtg	gag	gct	gag	gat	gtt	ggg	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	

100	105	110	
tgc atg caa gct cga caa act cca ttc act ttc ggc cct ggg acc aaa			384
Cys Met Gln Ala Arg Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys			
115	120	125	
gtg gat atc aga cga act gtg gct gca cca tct gtc ttc atc ttc ccg			432
Val Asp Ile Arg Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
130	135	140	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg			480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
145	150	155	160
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat			528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
165	170	175	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac			576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
180	185	190	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa			624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
195	200	205	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag			672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
210	215	220	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag			720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *			
225	230	235	

&lt;210&gt; 2

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Light chain of CHIR-12.12 human anti-CD40 antibody

&lt;400&gt; 2

Met Ala Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Ser			
1	5	10	15
Gly Ser Ser Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Thr			
20	25	30	
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser			
35	40	45	
Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys			
50	55	60	
Pro Gly Gln Ser Pro Gln Val Leu Ile Ser Leu Gly Ser Asn Arg Ala			
65	70	75	80
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe			
85	90	95	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
100	105	110	
Cys Met Gln Ala Arg Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys			
115	120	125	
Val Asp Ile Arg Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
130	135	140	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
145	150	155	160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			

Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			180					185					190		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		195					200					205			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	210					215					220				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
225					230					235					

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<210> 3
<211> 2016
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Coding sequence for heavy chain of CHIR-12.12  
human anti-CD40 antibody (with introns)

<400> 3						
atggagtttg	ggctgagctg	ggttttcctt	gttgctat	taagaggtgt	ccagtgtcag	60
gtgcagtttg	tggagttctg	gggaggcgtg	gtccagcctg	ggaggtccct	gagactctcc	120
tgtgcagcct	ctggattcac	cttcagtagc	tatggcatgc	actgggtccg	ccagggtcca	180
ggcaaggggc	tggagttggg	ggcagttata	tcatatagag	aaagtaatag	ataccatgca	240
gactccgtga	agggccgatt	caccattctc	agagacaatt	ccaagatcac	gctgtatctg	300
caaatgaaca	gcctcagaac	tgaggacacg	gctgtgtatt	actgtgcgag	agatgggggt	360
atagcagcac	ctgggcctga	ctactggggc	cagggaaacc	tggtcacctg	ctcctcagca	420
agtaccaag	gccccatcgt	cttccccctg	gcgcccgcct	gcaagagcac	ctctgggggc	480
acagcggccc	tgggtctgct	ggccaaggac	tacttccccg	aaccgggtgac	ggtgtcgtgg	540
aactcaggcg	cctgtaccag	ggcgctgcac	accttccccg	ctgtcctaca	gtcctcagga	600
ctctactccc	tcagcagcgt	ggtgaccgtg	ccctccagca	gcttgggac	ccagacctac	660
atctgcaacg	tgaatcacaa	gcccagcaac	accaaggtgt	acaagagagt	tggtgagagg	720
ccagcacag	gagggagggg	gtctctgtga	agccaggctc	agcgctctgt	cttggaagca	780
tcccgctcat	gcagtcgcc	tcaggggcag	caaggcaggc	cccgctgccc	tcttcaccgc	840
gaggcctctg	cccgccccac	tcattgctcag	ggagagggtc	ttctggcttt	ttcccagggc	900
tctgggagc	cacaggctag	gtgcccctaa	cccaggccct	gcacacaaag	gggcagggtg	960
tgggctcaga	cctgccaaga	gccatatccg	ggaggaccct	gcccttgacc	taagcccacc	1020
caaaaggcca	aactctccac	tccctcagct	cggacacctt	ctctctctcc	agatttccag	1080
aactcccaat	ctctctctctg	cagagcccaa	atcttgtgac	aaaactcaca	catgccacc	1140
gtgccagggt	aagccagccc	aggcctcgcc	ctccagctca	aggcgggaca	ggtgccctag	1200
agtagcctgc	atccaggggac	aggccccagc	cgggtgctga	cacgtccacc	tccatctctt	1260
cctcagcacc	tgaactcctg	gggggacgct	cagctctcct	cttcccccca	aaacccaagg	1320
acacctctga	gatctcccgc	acctctgagg	tcacatgcgt	ggtgggtggac	gtgagccag	1380
aaagccctga	ggtaacagttc	aactggtagc	tggacggcgt	ggagggtgcat	aatgccaa	1440
caaaagccgcg	ggaggagcag	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	1500
tgcaccagga	ctggctgaat	ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	1560
cagcccccat	cgagaaaacc	atctccaaag	ccaaaggtgt	gacccgtggg	gtgcgagggc	1620
cacatggaca	gaggccgggt	cggcccaccc	ctgtgcccgt	gagtgaccgc	tgtaccaacc	1680
cttgtcccta	cagggcagcc	cgagaaaacca	caggtgtaca	ccctgcccc	atcccgggag	1740
gagatgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1800
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1860
gtgtctggact	ccgacggctc	cttcttctct	tatagcaagc	tcaccgtgga	caagagcagg	1920
tggcagcagg	ggaactgtct	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1980
accagaaaga	gcctctccct	cttcccqqct	aaatga			2016

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<210> 4
<211> 469
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Heavy chain of CHIR-12.12 human anti-CD40 antibody

<400> 4  
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Arg Gly

1	5	10	15
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln			
20	25	30	
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe			
35	40	45	
Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	
Glu Trp Val Ala Val Ile Ser Tyr Glu Glu Ser Asn Arg Tyr His Ala			
65	70	75	80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ile			
85	90	95	
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val			
100	105	110	
Tyr Tyr Cys Ala Arg Asp Gly Gly Ile Ala Ala Pro Gly Pro Asp Tyr			
115	120	125	
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly			
130	135	140	
Pro Ser Val Phe Pro Leu Ala Pro Ala Ser Lys Ser Thr Ser Gly Gly			
145	150	155	160
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val			
165	170	175	
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe			
180	185	190	
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Val Val			
195	200	205	
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val			
210	215	220	
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys			
225	230	235	240
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu			
245	250	255	
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr			
260	265	270	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val			
275	280	285	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val			
290	295	300	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser			
305	310	315	320
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
325	330	335	
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
340	345	350	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
355	360	365	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
370	375	380	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
385	390	395	400
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
405	410	415	
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
420	425	430	
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
435	440	445	
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
450	455	460	
Leu Ser Pro Gly Lys			
465			

&lt;210&gt; 5

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Heavy chain of variant of CHIR-12.12 human  
anti-CD40 antibody

&lt;400&gt; 5

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Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Arg Gly
 1          5          10          15
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
          20          25          30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
          35          40          45
Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
          50          55          60
Glu Trp Val Ala Val Ile Ser Tyr Glu Glu Ser Asn Arg Tyr His Ala
65          70          75          80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ile
          85          90          95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val
          100          105          110
Tyr Tyr Cys Ala Arg Asp Gly Gly Ile Ala Ala Pro Gly Pro Asp Tyr
          115          120          125
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
          130          135          140
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145          150          155          160
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
          165          170          175
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
          180          185          190
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
          195          200          205
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
          210          215          220
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
225          230          235          240
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
          245          250          255
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
          260          265          270
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
          275          280          285
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
          290          295          300
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305          310          315          320
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
          325          330          335
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
          340          345          350
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
          355          360          365
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
          370          375          380
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385          390          395          400
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
          405          410          415
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
          420          425          430
Thr Val Asp Lys Ser Arg Trp Gln Gly Asn Val Phe Ser Cys Ser
          435          440          445
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
          450          455          460
Leu Ser Pro Gly Lys
465

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<210> 6  
 <211> 239  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Light chain of CHIR-5.9 human anti-CD40 antibody

<400> 6  
 Met Ala Leu Leu Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Ser Gly Ala Ile Val Met Thr Gln Pro Pro Leu Ser Ser Pro  
 20 25 30  
 Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser  
 35 40 45  
 Leu Val His Ser Asp Gly Asn Thr Tyr Leu Asn Trp Leu Gln Gln Arg  
 50 55 60  
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Phe Phe Arg Arg Leu  
 65 70 75 80  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe  
 85 90 95  
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
 100 105 110  
 Cys Met Gln Val Thr Gln Phe Pro His Thr Phe Gly Gln Gly Thr Arg  
 115 120 125  
 Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
 130 135 140  
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
 145 150 155 160  
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
 165 170 175  
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 180 185 190  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 195 200 205  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
 210 215 220  
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 7  
 <211> 474  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Heavy chain of CHIR-5.9 human anti-CD40 antibody

<400> 7  
 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly  
 1 5 10 15  
 Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30  
 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe  
 35 40 45  
 Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser  
 65 70 75 80  
 Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser  
 85 90 95  
 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met  
 100 105 110  
 Tyr Tyr Cys Ala Arg Gly Thr Ala Ala Gly Arg Asp Tyr Tyr Tyr Tyr

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      115      120      125
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
      130      135      140
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ala Ser Lys
145      150      155      160
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      165      170      175
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      180      185      190
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      195      200      205
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
      210      215      220
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225      230      235      240
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
      245      250      255
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
      260      265      270
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
      275      280      285
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
      290      295      300
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305      310      315      320
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
      325      330      335
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
      340      345      350
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
      355      360      365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
      370      375      380
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385      390      395      400
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
      405      410      415
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
      420      425      430
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
      435      440      445
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
      450      455      460
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465      470

```

&lt;210&gt; 8

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Heavy chain of variant CHIR-5.9 human anti-CD40 antibody

&lt;400&gt; 8

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Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly
 1      5      10      15
Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      20      25      30
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
      35      40      45
Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
      50      55      60
Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser

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65          70          75          80
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
      85          90
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
      100      105      110
Tyr Tyr Cys Ala Arg Gly Thr Ala Ala Gly Arg Asp Tyr Tyr Tyr Tyr
      115      120      125
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
      130      135      140
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
      145      150      155      160
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      165      170      175
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      180      185      190
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      195      200      205
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
      210      215      220
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
      225      230      235      240
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
      245      250      255
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
      260      265      270
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
      275      280      285
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
      290      295      300
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
      305      310      315      320
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
      325      330      335
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
      340      345      350
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
      355      360      365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
      370      375      380
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
      385      390      395      400
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
      405      410      415
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
      420      425      430
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
      435      440      445
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
      450      455      460
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465          470

```

&lt;210&gt; 9

&lt;211&gt; 612

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(612)

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Coding sequence for short isoform of human CD40



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<400> 9
atg gtt cgt ctg cct ctg cag tgc gtc ctc tgg ggc tgc ttg ctg acc 48
Met Val Arg Leu Pro Leu Gln Cys Val Leu Trp Gly Cys Leu Leu Thr
1 5 10 15

gct gtc cat cca gaa cca ccc act gca tgc aga gaa aaa cag tac cta 96
Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
20 25 30

ata aac agt cag tgc tgt tct ttg tgc cag cca gga cag aaa ctg gtg 144
Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
35 40 45

agt gac tgc aca gag ttc act gaa acg gaa tgc ctt cct tgc ggt gaa 192
Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
50 55 60

agc gaa ttc cta gac acc tgg aac aga gag aca cac tgc cac cag cac 240
Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
65 70 75 80

aaa tac tgc gac ccc aac cta ggg ctt cgg gtc cag cag aag ggc acc 288
Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
85 90 95

tca gaa aca gac acc atc tgc acc tgt gaa gaa ggc tgg cac tgt acg 336
Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
100 105 110

agt gag gcc tgt gag agc tgt gtc ctg cac cgc tca tgc tcg ccc ggc 384
Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
115 120 125

ttt ggg gtc aag cag att gct aca ggg gtt tct gat acc atc tgc gag 432
Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
130 135 140

ccc tgc cca gtc ggc ttc ttc tcc aat gtg tca tct gct ttc gaa aaa 480
Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
145 150 155 160

tgt cac cct tgg aca agg tcc cca gga tcg gct gag agc cct ggt ggt 528
Cys His Pro Trp Thr Arg Ser Pro Gly Ser Ala Glu Ser Pro Gly Gly
165 170 175

gat ccc cat cat ctt cgg gat cct gtt tgc cat cct ctt ggt gct ggt 576
Asp Pro His His Leu Arg Asp Pro Val Cys His Pro Leu Gly Ala Gly
180 185 190

ctt tat caa aaa ggt ggc caa gaa gcc aac caa taa 612
Leu Tyr Gln Lys Gly Gly Gln Glu Ala Asn Gln *
195 200

```

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<210> 10
<211> 203
<212> PRT
<213> Homo sapiens

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<400> 10
Met Val Arg Leu Pro Leu Gln Cys Val Leu Trp Gly Cys Leu Leu Thr
1 5 10 15
Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
20 25 30
Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
35 40 45

```

```

Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
 50          55          60
Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
 65          70          75          80
Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
          85          90          95
Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
          100          105          110
Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
          115          120          125
Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
          130          135          140
Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
          145          150          155          160
Cys His Pro Trp Thr Arg Ser Pro Gly Ser Ala Glu Ser Pro Gly Gly
          165          170          175          180
Asp Pro His His Leu Arg Asp Pro Val Cys His Pro Leu Gly Ala Gly
          180          185          190          195
Leu Tyr Gln Lys Gly Gly Gln Glu Ala Asn Gln
          195          200

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&lt;210&gt; 11

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(834)

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Coding sequence for long isoform of human CD40

&lt;400&gt; 11

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atg gtt cgt ctg cct ctg cag tgc gtc ctc tgg ggc tgc ttg ctg acc 48
Met Val Arg Leu Pro Leu Gln Cys Val Leu Trp Gly Cys Leu Leu Thr
 1          5          10          15

gct gtc cat cca gaa cca ccc act gca tgc aga gaa aaa cag tac cta 96
Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
          20          25          30

ata aac agt cag tgc tgt tct ttg tgc cag cca gga cag aaa ctg gtg 144
Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
          35          40          45

agt gac tgc aca gag ttc act gaa acg gaa tgc ctt cct tgc ggt gaa 192
Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
          50          55          60

agc gaa ttc cta gac acc tgg aac aga gag aca cac tgc cac cag cac 240
Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
          65          70          75          80

aaa tac tgc gac ccc aac cta ggg ctt cgg gtc cag cag aag ggc acc 288
Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
          85          90          95

tca gaa aca gac acc atc tgc acc tgt gaa gaa ggc tgg cac tgt acg 336
Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
          100          105          110

agt gag gcc tgt gag agc tgt gtc ctg cac cgc tca tgc tcg ccc ggc 384
Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly

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115	120	125	
ttt ggg gtc aag cag att gct	aca ggg gtt tct gat acc atc tgc gag	432	
Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu			
130	135	140	
ccc tgc cca gtc ggc ttc ttc tcc aat gtg tca tct gct ttc gaa aaa	480		
Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys			
145	150	155	
tgt cac cct tgg aca agc tgt gag acc aaa gac ctg gtt gtg caa cag	528		
Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln			
165	170	175	
gca ggc aca aac aag act gat gtt gtc tgt ggt ccc cag gat cgg ctg	576		
Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu			
180	185	190	
aga gcc ctg gtg gtg atc ccc atc atc ttc ggg atc ctg ttt gcc atc	624		
Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile			
195	200	205	
ctc ttg gtg ctg gtc ttt atc aaa aag gtg gcc aag aag cca acc aat	672		
Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn			
210	215	220	
aag gcc ccc cac ccc aag cag gaa ccc cag gag atc aat ttt ccc gac	720		
Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp			
225	230	235	
gat ctt cct ggc tcc aac act gct gct cca gtg cag gag act tta cat	768		
Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His			
245	250	255	
gga tgc caa ccg gtc acc cag gag gat ggc aaa gag agt cgc atc tca	816		
Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser			
260	265	270	
gtg cag gag aga cag tga	834		
Val Gln Glu Arg Gln *			
275			

&lt;210&gt; 12

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

Met Val Arg Leu Pro Leu Gln Cys Val Leu Trp Gly Cys Leu Leu Thr	
1 5 10 15	
Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu	
20 25 30	
Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val	
35 40 45	
Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu	
50 55 60	
Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His	
65 70 75 80	
Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr	
85 90 95	
Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr	
100 105 110	
Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly	
115 120 125	
Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu	

130					135					140					
Pro	Cys	Pro	Val	Gly	Phe	Phe	Ser	Asn	Val	Ser	Ser	Ala	Phe	Glu	Lys
145					150					155					160
Cys	His	Pro	Trp	Thr	Ser	Cys	Glu	Thr	Lys	Asp	Leu	Val	Val	Gln	Gln
				165					170						175
Ala	Gly	Thr	Asn	Lys	Thr	Asp	Val	Val	Cys	Gly	Pro	Gln	Asp	Arg	Leu
			180					185					190		
Arg	Ala	Leu	Val	Val	Ile	Pro	Ile	Ile	Phe	Gly	Ile	Leu	Phe	Ala	Ile
		195					200					205			
Leu	Leu	Val	Leu	Val	Phe	Ile	Lys	Lys	Val	Ala	Lys	Lys	Pro	Thr	Asn
	210					215					220				
Lys	Ala	Pro	His	Pro	Lys	Gln	Glu	Pro	Gln	Glu	Ile	Asn	Phe	Pro	Asp
225					230					235					240
Asp	Leu	Pro	Gly	Ser	Asn	Thr	Ala	Ala	Pro	Val	Gln	Glu	Thr	Leu	His
				245					250						255
Gly	Cys	Gln	Pro	Val	Thr	Gln	Glu	Asp	Gly	Lys	Glu	Ser	Arg	Ile	Ser
			260					265					270		
Val	Gln	Glu	Arg	Gln											
			275												